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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/724,584	11/28/2000	Kenneth W. Wood	UCSD-04870	9473

23535 7590 10/22/2002

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EXAMINER	
HOLLERAN, ANNE L	
ART UNIT	PAPER NUMBER
1642	10

DATE MAILED: 10/22/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No. 09/724,584	Applicant(s) WOOD ET AL.	
	Examiner Anne Holleran	Art Unit 1642	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *02 May 2002* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-42* is/are pending in the application.

4a) Of the above claim(s) *1-11,16-38 and 40-42* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *12-15 and 39* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *4* .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

1. Applicant's election without traverse of Group 2, claims 12-15 and 39 in Paper No. 8 (filed May 2, 2002) is acknowledged.

Claims 1-42 are pending.

Claims 1-11, 16-38 and 40-42, drawn to non-elected inventions, are withdrawn from consideration.

Claims 12-15 and 39 are examined on the merits.

Objection to the Specification:

2. The specification is objected to because the application is not in compliance with the sequence rules asset forth in 37 CFR 1.821(a)(1) and (a)(2). The application fails to contain a computer readable form (CRF) of the sequence listing, and there is no statement from applicant to transfer the CRF from a parent application to this application.

Applicant is given the time period for reply to this Office action to comply with the requirements of 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Sample Request to Use Computer Readable Form from Another Application

The following paragraph, or language having the same effect, can be used to invoke the procedures of 37 CFR section 1.821(e) in which an identical computer readable form (CRF) from another application should be incorporated into a separate paper to be submitted in the given application:

> The computer readable form (CRF) in this application, 08/100,000, is identical with that filed in parent application, 07/999,999, filed March 1, 1988. In accordance with 37 CFR 1.821(e), please use the **[first-filed, last-filed or only, whichever is applicable]** CRF of 07/999,999 as the CRF for the instant application. It is understood that the Patent and Trademark Office will make the necessary changes in the application number and filing date for the CRF that will be used for the instant application. A paper copy of the Sequence Listing is **[included in the originally-filed specification of the instant application, included in the separately filed preliminary amendment for incorporation into the specification, whichever is applicable]**.

Claim Rejections - 35 USC § 112

3. Claims 12-15 and 39 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 12 is indefinite because of the percent identity language where a protein is described as having greater than 70 percent amino acid sequence identity to a protein whose amino acid sequence is not recited in the claims.

Claims 12 and 39 are indefinite because they contain the abbreviation CENP-E. An abbreviation must be accompanied by the full name at its first occurrence in the claims.

4. Claims 12, 14, and 15 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for nucleic acid sequences that encode the amino acid

sequence of SEQ ID NO: 1, or encode a protein comprising the amino acids sequence of 1-324 of SEQ ID NO: 1, does not reasonably provide enablement for the full scope of nucleic acid sequences encoding proteins comprising core motor domains having at least 70 percent amino acid sequence identity to a Xenopus CENP-E core motor domain, which proteins specifically bind to antibodies raised against CENP-E. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims.

Factors to be considered in determining whether undue experimentation would be required to practice the full scope of the claimed inventions are: 1) quantity of experimentation necessary; 2) the amount of direction or guidance presented in the specification; 3) the presence or absence of working examples; 4) the nature of the invention; 5) the state of the prior art; 6) the relative skill of those in the art; 7) the predictability or unpredictability of the art; and 8) the breadth of the claims. See Ex parte Forman, 230 USPQ 546, BPAI, 1986.

Claims 12, 14 and 15 are drawn to nucleic acid sequences that encode proteins comprising regions that have greater than 70 percent amino acid sequence identity to a Xenopus CENP-E core motor domain. The limitation that the encoded proteins specifically bind to antibodies raised against CENP-E does not limit the scope to what is enabled by the specification, because proteins having widely varying functions may share immunological epitopes. Furthermore, an immunological epitope represents only a very small portion of an entire protein structure. Thus, the claims are drawn to a genus of nucleic acid molecules that encode a widely varying genus of protein molecules, and the claims are drawn to nucleic acids that encode proteins that would not have the same function as that of the exemplified protein.

The specification teaches one example of a protein that is a Xenopus CENP-E protein that comprises a motor domain. The specification contemplates variants of this sequence, but fails to provide examples of such proteins and fails to provide guidance for how to use structural variants of the exemplified protein. Such guidance is necessary because the relationship between the primary amino acid sequence and protein function is highly unpredictable. Bowie et al (Science, 247: 1306-1310, 1990) teaches that while it is known that many amino acid substitutions are possible in any given protein, the position with the protein sequence where such amino acid substitutions can be made with a reasonable expectation of maintaining function are limited. Burgess et al (J. Cell Biology, 111: 2129-2138, 1990) teaches that replacement of a single lysine residue at position 118 of acidic fibroblast growth factor by glutamic acid led to the substantial loss of heparin binding, receptor binding and biological activity of the protein. Lazar et al (Molecular and Cellular Biology, 8: 1247-1252, 1988) teaches that replacement of aspartic acid at position 47 with alanine or asparagines does not affect biological activity while replacement with serine or glutamic acid sharply reduces the biological activity of the protein. These references demonstrate that even a single amino acid substitution will often dramatically affect the biological activity and characteristics of a protein.

Because of the broad scope of the claims that is not commensurate in scope with that of the disclosure of the specification, and in view of the unpredictability of protein chemistry, undue experimentation on the part of one skilled in the art would be necessary to practice the full scope the claimed invention. Without knowledge of the function of the encoded proteins, one of skill in the art would not know how to use the proteins encoded by the claimed nucleic acids and

therefore, would not know how to use the claimed nucleic acids for anything other than experimentation on the nucleic acids themselves or the proteins encoded thereby.

5. Claims 12, 14, 15 and 39 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The basis for this rejection is that specification fails to provide adequate written description of the genus of proteins referred to as CENP-E gene product, Xenopus CENP-E, CENP-E, or CENP-E polypeptide.

The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. See University of California v. Eli Lilly and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). The court state that "[a] written description of an invention involving a chemical genus, like a description of a chemical species, 'requires a precise definition, such as by structure, formula, [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials." Id. at 1567, 43 USPQ2d at 1405. The court also addressed the manner by which a genus of cDNAs might be described. "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." Id.

The specification describes the sequence of one example of a Xenopus CENP-E and the sequence of a human CENP-E, but fails to describe the sequences of any variants of either of these sequences, and fails to describe how these sequences are representative of the genus of sequences represented by the terms CENP-E gene product, Xenopus CENP-E, CENP-E, or CENP-E polypeptide. Thus, the specification fails to provide either a "representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus, or a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." See Lilly, 119 F.3d at 1568, 43 USPQ2d at 1406. Nor does the specification otherwise allow a skilled artisan to "visualize or recognize the identity of the members of the genus." See id. Therefore, the specification does not adequately describe the genus of polynucleotides encoding polypeptides that may broadly be referred to as CENP-E gene product, Xenopus CENP-E, CENP-E, or CENP-E polypeptide. Therefore, the specification does not adequately describe the genus recited in the claims, nor does the specification adequate describe the methods of making a genus of biologically active CENP-E.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

6. Claims 12, 14, and 15 are rejected under 35 U.S.C. 102(b) as being rejected by Yen (Yen, T.J., et al, Nature, 359: 536-539, 1992; cited in the IDS).

Yen teaches a human CENP-E nucleic acid sequence that encodes a protein which has greater than 70 percent identity to amino acids 1-324 of SEQ ID NO: 1, the amino acid sequence of a Xenopus CENP-E motore domain (see sequence alignment). Yen teaches that the encoded protein has a molecular weight of 312kDa. Thus, Yen teaches a nucleic acid sequence that is the same as that claimed.

The limitation of claim 14, that the comparison algorithm is PILEUP, is met by Yen, because no algorithm parameters are cited in the claim. Absent evidence to the contrary, it is believed that there exist at least one set of alorithm parameters of PILEUP where the alignment between a Xenopus CENP-E core motor domain and the sequence of Yen would result in a match that is greater than 70 percent identity.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

The factual inquiries set forth in *Graham* v. *John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.

2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

7. Claim 39 is rejected under 35 U.S.C. 103(a) as being unpatentable over Brown (Brown, K.D, et al, J. Cell Biology, 125: 13003-1312, 1994) in view of Hyman (Hyman and Mitchison, Nature, 351: 206-211, 1991; cited in the IDS).

Claim 39 is drawn to a method of producing a biologically active CENP-E polypeptide comprising transforming a cell with nucleic acid sequence encoding a motor domain of CENP-E, expressing the nucleic acid, purifying the gene product and identifying ATPase activity or plus-end directed microtubule activity of the gene product.

Brown teaches a method of making a recombinant human CENP-E in baculovirus expression system. Brown fails to teach further assaying the expressed protein for ATPase activity or plus-end directed microtubule activity. However, an assay for ATPase activity for CENP-E is known in the art, as taught by Hyman. An assay for ATPase activity is used to assess motor activity of a CENP-E protein. Thus, it would have been prima facie obvious to

one of skill in the art at the time the invention was made to have made a method for producing a biologically active CENP-E polypeptide. One would have been motivated to have combined the teachings of Brown with Hyman because it is routine in the art of protein expression to assay for function of a recombinant protein.

Conclusion

No claim is allowed. Claim 13 is free of the prior art.

Any inquiry concerning this communication or earlier communications from the Office should be directed to Anne Holleran, Ph.D. whose telephone number is (703) 308-8892. Examiner Holleran can normally be reached Monday through Friday, 9:30 am to 2:30 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anthony Caputa, Ph.D. can be reached at (703) 308-3995.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist at telephone number (703) 308-0196.

Anne L. Holleran
Patent Examiner
October 19, 2002

ANTHONY C. CAPUTA
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Notice to Comply With Sequence Rules	Application No. 09/724,584	Applicant(s) WOOD ET AL.
	Examiner Anne Holleran	Art Unit 1642

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

X 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 8230, May 1, 1990.

___ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

X 3. A copy of the "Sequence Listing" in Computer Readable Form (CRF) has not been submitted as required by 37 C.F.R. 1.821(e).

___ 4. A copy of the "Sequence Listing" in Computer Readable Form (CRF) has been submitted. However, the content of the CRF does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

___ 5. The Computer Readable Form (CRF) that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute CRF must be submitted as required by 37 C.F.R. 1.825(d).

___ 6. The paper copy of the "Sequence Listing" is not the same as the Computer Readable Form (CRF) of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

X 7. Other: Application lacks statement that CRF of parent may be used in this application

Applicant Must Provide:

X An initial or substitute copy of the **CRF** "Sequence Listing". (or a request to transfer CRF from parent file).

___ An initial or substitute **paper copy** of the "Sequence Listing", as well as an amendment directing its entry into the specification.

X A statement that the content of the paper and CRF copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support (SIRA)
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Jul 28 14:52:34 2000; MasPar time 12.47 Seconds
804.863 Million cell updates/sec

Tabular output not generated.

Title: >US-09-150-867-1
Description: (1-324) from US09150867.pep (2 of 2)
Perfect Score: 2288
Sequence: 1 MSEGDAVKVCVRVRPLIQRE.....IICTITPVSFDETLSTLQFA 324

Scoring table: PAM 150
Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 49.270; Variance 88.569; scale 0.556

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1754	76.7	2663	1	CENE_HUMAN	CENTROMERIC PROTEIN E	0.00e+00
2	852	37.2	742	1	KI21_STRPU	KINESIN-II 95 KDA SUBU	3.91e-158
3	847	37.0	747	1	KF3B_HUMAN	KINESIN-LIKE PROTEIN K	5.40e-157
4	847	37.0	747	1	KF3B_MOUSE	KINESIN-LIKE PROTEIN K	5.40e-157
5	840	36.7	699	1	KI22_STRPU	KINESIN-II 85 KDA SUBU	2.13e-155
6	832	36.4	1231	1	KIF4_MOUSE	KINESIN-LIKE PROTEIN K	1.42e-153
7	824	36.0	701	1	KF3A_MOUSE	KINESIN-LIKE PROTEIN K	9.43e-152
8	823	36.0	702	1	KF3A_HUMAN	KINESIN-LIKE PROTEIN K	1.59e-151
9	820	35.8	786	1	FL10_CHLRE	KINESIN-LIKE PROTEIN F	7.68e-151
10	815	35.6	1232	1	KIF4_HUMAN	KINESIN-LIKE PROTEIN K	1.05e-149
11	807	35.3	1031	1	KINH_STRPU	KINESIN HEAVY CHAIN.	6.97e-148
12	804	35.1	963	1	KINH_HUMAN	KINESIN HEAVY CHAIN (U	3.35e-147
13	804	35.1	963	1	KINH_MOUSE	KINESIN HEAVY CHAIN (U	3.35e-147
14	794	34.7	975	1	KINH_DROME	KINESIN HEAVY CHAIN.	6.28e-145
15	786	34.4	815	1	KINH_CAEEL	KINESIN HEAVY CHAIN.	4.12e-143
16	787	34.4	928	1	KINH_NEUCR	KINESIN HEAVY CHAIN.	2.44e-143
17	780	34.1	1032	1	KINN_HUMAN	NEURONAL KINESIN HEAVY	9.48e-142
18	778	34.0	672	1	OSM3_CAEEL	KINESIN-LIKE PROTEIN O	2.69e-141
19	775	33.9	967	1	KINH_LOLPE	KINESIN HEAVY CHAIN.	1.29e-140
20	765	33.4	1027	1	KINN_MOUSE	NEURONAL KINESIN HEAVY	2.39e-138
21	738	32.3	784	1	KL68_DROME	KINESIN-LIKE PROTEIN K	3.09e-132
22	709	31.0	805	1	YGW6_YEAST	PUTATIVE KINESIN-LIKE	1.09e-125
23	708	30.9	935	1	KINH_SYNRA	KINESIN HEAVY CHAIN (S	1.84e-125
24	703	30.7	883	1	YB3D_SCHPO	PUTATIVE KINESIN-LIKE	2.46e-124
25	695	30.4	1103	1	KF1C_HUMAN	KINESIN-LIKE PROTEIN K	1.56e-122
26	696	30.4	1584	1	U104_CAEEL	KINESIN-LIKE PROTEIN U	9.28e-123
27	691	30.2	1150	1	KF1B_MOUSE	KINESIN-LIKE PROTEIN K	1.24e-121
28	651	28.5	1690	1	KF1A_HUMAN	KINESIN-LIKE PROTEIN K	1.19e-112
29	649	28.4	1695	1	KF1A_MOUSE	KINESIN-LIKE PROTEIN K	3.33e-112
30	642	28.1	378	1	KLP2_BOMMO	KINESIN-LIKE PROTEIN K	1.23e-110
31	644	28.1	770	1	KLPA_EMENI	KINESIN-LIKE PROTEIN K	4.39e-111
32	640	28.0	1066	1	KL61_DROME	BIPOLAR KINESIN KRP-13	3.45e-110
33	638	27.9	776	1	KLP1_CHLRE	KINESIN-LIKE PROTEIN K	9.66e-110
34	629	27.5	1184	1	BIMC_EMENI	KINESIN-LIKE PROTEIN B	9.93e-108
35	616	26.9	700	1	NCD_DROME	CLARET SEGREGATIONAL P	7.92e-105
36	612	26.7	643	1	CTK2_XENLA	CARBOXY-TERMINAL KINES	6.18e-104
37	607	26.5	793	1	KF3C_HUMAN	KINESIN-LIKE PROTEIN K	8.03e-103
38	603	26.4	1085	1	CUT7_SCHPO	KINESIN-LIKE PROTEIN C	6.25e-102
39	601	26.3	1067	1	EG52_XENLA	KINESIN-LIKE PROTEIN E	1.74e-101
40	598	26.1	796	1	KF3C_MOUSE	KINESIN-LIKE PROTEIN K	8.10e-101
41	594	26.0	1057	1	EG5_HUMAN	KINESIN-RELATED MOTOR	6.28e-100
42	590	25.8	796	1	KF3C_RAT	KINESIN-LIKE PROTEIN K	4.87e-99
43	584	25.5	1060	1	EG51_XENLA	KINESIN-RELATED MOTOR	1.05e-97
44	566	24.7	598	1	KLP3_CAEEL	KINESIN-LIKE PROTEIN K	1.03e-93
45	564	24.7	754	1	KATC_ARATH	KINESIN-LIKE PROTEIN C	2.84e-93

ALIGNMENTS

```
RESULT    1
ID   CENE_HUMAN     STANDARD;      PRT;  2663 AA.
AC   Q02224;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-FEB-2000 (Rel. 39, Last annotation update)
DE   CENTROMERIC PROTEIN E (CENP-E PROTEIN).
GN   CENPE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93024922.
RA   Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
RT   "CENP-E is a putative kinetochore motor that accumulates just before
RT   mitosis.";
RL   Nature 359:536-539(1992).
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE; 95196755.
RA   Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
RT   "Mitotic HeLa cells contain a CENP-E-associated minus end-directed
RT   microtubule motor.";
RL   EMBO J. 14:918-926(1995).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE; 98437347.
RA   Chan G.K.T., Schaar B.T., Yen T.J.;
RT   "Characterization of the kinetochore binding domain of CENP-E reveals
RT   interactions with the kinetochore proteins CENP-F and hBUBR1.";
RL   J. Cell Biol. 143:49-63(1998).
CC   -!- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE
CC       KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE
CC       OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT
CC       AND/OR SPINDLE ELONGATION.
CC   -!- SUBUNIT: INTERACTS WITH CENP-F AND BUBR1 KINASE.
CC   -!- SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CC       CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS
CC       QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
CC   -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; Z15005; CAA78727.1; -.
DR   PIR; S28261; S28261.
DR   HSSP; P03069; 12II.
DR   MIM; 117143; -.
DR   PFAM; PF00225; kinesin; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW   Motor protein; Cell division; ATP-binding; Coiled coil; Mitosis;
KW   Cell cycle; Centromere.
FT   DOMAIN        1    335       MECHANOCHEMICAL (MOTOR).
FT   DOMAIN      336   2471       COILED COIL (POTENTIAL).
FT   DOMAIN     2472   2663       GLOBULAR (POTENTIAL).
FT   NP_BIND      86     93       ATP (BY SIMILARITY).
SQ   SEQUENCE   2663 AA;  312087 MW;  CEFC13880C8C8CB8 CRC64;

  Query Match           76.7%;  Score 1754;  DB 1;  Length 2663;
  Best Local Similarity 73.9%;  Pred. No. 0.00e+00;
  Matches  241;  Conservative   44;  Mismatches  36;  Indels   5;  Gaps   3;

Db       1 MAEEGAVAVCVRVRPLNSREESLGETAQVYWKTDNNVIYQVDGSKSFNFDRVFHGNETTK 60
           |:|  || |||||||| ||:  |: | : ||: || | ||||:||||||||:::|:|
Qy       1 MSEGDAVKVCVRVRPLIQREQ--GDQANLQWKAGNNTISQVDGTKSFNFDRVFNSHESTS 58

Db      61 NVYEEIAAPIIDSAIQGYNGTIFAYGQTASGKTYTMMGSEDHLGVIPRAIHDIFQKIKKF 120
           :|:||| ||| ||:|||||||||||||:|||||||||: : ||:||:||:::|  |  :
Qy      59 QIYQEIAVPIIRSALQGYNGTIFAYGQTSSGKTYTMMGTPNSLGIIPQAIQEVFKIIQEI 118

Db     121 PDREFLLRVSYMEIYNETITDLLCGTQKMKPLIIREDVNRNVYVADLTEEVVYTSEMALK 180
           |:|||||||||||||||: |||| :::||| |||| ||||||||||||:|  :|  :
Qy     119 PNREFLLRVSYMEIYNETVKDLLCDDRRKKPLEIREDFNRNVYVADLTEELVMVPEHVIQ 178

Db     181 WITKGEKSRHYGETKMNQRSSRSHTIFRMILESREKGEP--S-NCEGSVKVSHLNLVDLA 237
           || ||||:|||||||||::|||||||||||:|||:: :|  | ||:|:|:|||||||||
Qy     179 WIKKGEKNRHYGETKMNDHSSRSHTIFRMIVESRDRNDPTNSENCDGAVMVSHLNLVDLA 238

Db     238 GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFINYRDSKLTRILQNSLG 297
           |||||:|||| ||||||||||||||||||||||||||| ||||||||||||||||||||
Qy     239 GSERASQTGAEGVRLKEGCNINRSLFILGQVIKKLSDGQAGGFINYRDSKLTRILQNSLG 298

Db     298 GNPKTRIICTITPVSFDETLTALQFA 323
           ||:|| ||||||||||||||::||||
Qy     299 GNAKTVIICTITPVSFDETLSTLQFA 324
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RESULT    2
ID   KI21_STRPU     STANDARD;      PRT;   742 AA.
AC   P46871;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   KINESIN-II 95 KDA SUBUNIT (KRP-85/95 95 KDA SUBUNIT).
GN   KRP95.
OS   Strongylocentrotus purpuratus (Purple sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
OC   Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC   Strongylocentrotus.
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=EGG;
RX   MEDLINE; 94050179.
RA   Cole D.G., Chinn S.W., Wedaman K.P., Hall K., Vuong T.,
RA   Scholey J.M.;
RT   "Novel heterotrimeric kinesin-related protein purified from sea
RT   urchin eggs.";
RL   Nature 366:268-270(1993).
CC   -!- SUBUNIT: TRIMER OF A 115 KDA SUBUNIT AND TWO KINESIN-LIKE SUBUNITS
CC       OF 95 AND 85 KDA.
CC   -!- PTM: THE N-TERMINUS IS BLOCKED.
CC   -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
CC       II SUBFAMILY.
CC   ------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; U00996; AAA87393.1; -.
DR   HSSP; P56536; 2KIN.
DR   PFAM; PF00225; kinesin; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW   Motor protein; Microtubules; ATP-binding; Coiled coil.
FT   DOMAIN        1    337       MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
FT   DOMAIN      338    613       COILED COIL (BY SIMILARITY).
FT   DOMAIN      614    742       GLOBULAR (BY SIMILARITY).
FT   NP_BIND      95    102       ATP (POTENTIAL).
SQ   SEQUENCE   742 AA;  84202 MW;  47C40A367BAA77B5 CRC64;

  Query Match           37.2%;  Score 852;  DB 1;  Length 742;
  Best Local Similarity 47.1%;  Pred. No. 3.91e-158;
  Matches  137;  Conservative   66;  Mismatches  74;  Indels  14;  Gaps  11;

Db      51 EPNKSFTFDTVYDWNSKQIDLYDETFRSLVESVLQGFNGTIFAYGQTGTGKTFTMEGVRS 110
           :  ||| || |:: :    ::|:|   ::: | |||:||||||||||::|||:|| |  :
Qy      40 DGTKSFNFDRVFNSHESTSQIYQEIAVPIIRSALQGYNGTIFAYGQTSSGKTYTMMGT-P 98

Db     111 NPELRGVIPNSFEHIFTHIARTQNQQFLVRASYLEIYQEEIRDLLAKDQKKR-LDLKERP 169
           |: | |:|| ::: :|  |    |::||:| ||:||| | ::|||  |::|: |:::|
Qy      99 NS-L-GIIPQAIQEVFKIIQEIPNREFLLRVSYMEIYNETVKDLLCDDRRKKPLEIREDF 156

Db     170 DTGVYVKDLSS-FVTKSVKEIEHVMTVGNNNRSVGSTNMNEHSSRSHAIFIITIECSELG 228
           :  ||| ||:  :|  :   |: ::  |::||  | |:||:|||||:|| : :|  :
Qy     157 NRNVYVADLTEELVMVPEHVIQWIKK-GEKNRHYGETKMNDHSSRSHTIFRMIVESRDRN 215

Db     229 --VDGEN-H--IRVGKLNLVDLAGSERQAKTGATGDRLKEATKINLSLSALGNVISALVD 283
             ::||    : |: ||||||||||| : ||| | ||||: :|| ||  || ||  | |
Qy     216 DPTNSENCDGAVMVSHLNLVDLAGSERASQTGAEGVRLKEGCNINRSLFILGQVIKKLSD 275

Db     284 GKSS-HIPYRDSKLTRLLQDSLGGNAKTVMVANMGPASYNFDETITTLRYA 333
           | ::  | ||||||||:||:||||||||||::  : | |  ||||::||::|
Qy     276 GQAGGFINYRDSKLTRILQNSLGGNAKTVIICTITPVS--FDETLSTLQFA 324
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RESULT    3
ID   KF3B_HUMAN     STANDARD;      PRT;   747 AA.
AC   O15066;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   KINESIN-LIKE PROTEIN KIF3B (MICROTUBULE PLUS END-DIRECTED KINESIN
DE   MOTOR 3B) (KIAA0359) (HH0048).
GN   KIF3B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 97349984.
RA   Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA   Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. VII.
RT   The complete sequences of 100 new cDNA clones from brain which can
RT   code for large proteins in vitro.";
RL   DNA Res. 4:141-150(1997).
CC   -!- FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR
CC       MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE SLIDING
CC       ACTIVITY IN VITRO (BY SIMILARITY).
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